

GGGGGGGGGGGGGTCAGAGGGAGCTTCTTTAGGCCGTCCATCTGTGAAT
 CTAACCTCAGTTCTGGGAATCAGGAAGCATGCATCTCCTCTTAGTCAGCTG
 CTTGTTCTCTGGCTCTGGGAAGGCAGACCTATGTGTGGATGGCTGCCAGAG
 TCAGGGCTCTTATCCTTCCTCTAGAAAGGGTTCGCAGAGATCTCCACG
 TGGCCAACCACGAGGAGGCAGAAGACAAGCCGATCTGTTGTGGCCGTGCCA
 CACCTCATGGGCACCAGCCTGGCTGGGAAGGCCAGAGGCAGAGAGGGAAAGAT
 GCTGTCCAGGCTTGAAGATTCTGGAAGAAACCTGAGACCGAATTTCACCCCC
 CAAGGGATGTGGAAAGCGATCATGTCTCATCGGGATGCAGGCCGTGACTCAG
 CCAGCAGATGGGAGGAAAGTGGAGAGATCACCTCTACAGGAGGAAGCCAAGAG
 GTTCTGGCATCGGTCATGTTAGAAAGGGCCGGCGTCCAGGGAGTCATCC
 TGCCCATCAAAAGCCACGAAGTACACTGGGAGACCTGCAGGACTGTGCCCTTC
 AACCAAGACCATGCCATGAAGACTGTCAAAAGTCGTTGTCCAGAACAAACCT
 TTGCTTGGCAAATGCAGTTCCATTGTTCCGGAGAAGGGCAGATGCC
 ACAGCTTCTGCTCCCAGTGCCTGCCACCAATTACCCACCGTGCACTTGATG
 CTGAACGTGACCCAGCCCAACCCCGTGGTCAAGATGGTATGCAAGTAGAAGA
 GTGTCAGTGCATGGTGAAGACGGAACGTGGAGAGGAGGCCTCCTACTGGCTG
 GTTCCCAGGGTCTTCATCCCTGGACTTCAGCTTCAAAACAAACCCATGA
 ATTACCTCAACAGAAAGCAAACCTCAACAGAATAAGTGAGGGTTATTCAATC
 TGGAAATGTTATGTGAGTTATATAAGATCAGTGGAAAATATCTTCTCTCTC
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 GTGGCTGGGATGATTAAACTCCTGATCCAATTCTGAGTGCTGGGATTAC
 AGACATGCTCCATAANACATAGCTCCAGAAGGATTAAAGAGATTG
 ATGTTCAAAGTTGCCTTGAGACTCAGAAATATTTGATNTATTGAATGGCC
 TTGCCACAGATGTGGGAGGCAGCTGCTGGTGGCCCAAGTATTTTTTTG
 TTCGTTAGAATTCTCACATGAAGTTTACTGTTGGTTATCTGGCGTTGAA
 GAAGGAATAGTGAAGGTACTTTAACAGTTACACGTGGAAGGGCTCAGGCA
 CTAGGAACCAACCTTCCCGGAATATGAGGAAATACATGAACAGTATTAGA
 GTCACTTGAGGAAGTTACTAGGAAACGCCATAAGTCTCCAAGTACATTGTGAG
 TCATTTGAAGGACAATCGTGTATATAGACGAAATCTCTACTCGTATGCTTT
 TGAATCTCTAGCAAGTTAGGTTCTATGTTGGGCTCTCTATTGTCTAA
 GAGTATGTGTGACAAATTCAACCTGACAAATACCTCAATGGCAAATTCTGACC
 CTG (SEQ ID NO: 22)

MHLLLVQLLVLLPLGKADLCVDGCQSQGSLSFPLLERGRRLHVANHEEAEDK
 PDLFVAVPHLMGTSLAGEGQRQRGKMLSRLGRFWKKPETEFYPPRDVESDHVS
 SGMQAVTQPADGRKVERSPLQEEAKRFWHRFMFRKGPAFQGVILPIKSHEVHW
 ETCRTVPFNQTIAHEDCQKVQQNNLCFGKCSSIRFPGEGADAHSFCSHCSPT
 KFTTVHMLNCTSPTPVVKMVMQVEECQCMVKTERGEERLLLALGSQGSFIPGL
 PASKTNP (SEQ ID NO: 22)

FIGURE 1

Construct

Gene: 67

GI Number(s): 6753409

Gene Family: Growth Factor Inhibitor

Gene Subfamily: Cerberus

Gene Sequence: full-length cDNA, Mouse

underlined = deleted in targeting construct

[] = sequence flanking Neo insert in targeting construct

[GGGGGGGGGGGGGGTCAGAGGGAGCTTCTTTAGGCCGTCCATCTGTGAATCTAACCTCAGTTCTGGGAATCAGGAAGCATGCATCTCCTCTAGTCAGCTGCTGTCTCTGCCTCTGGGAAGGCAGACCTATGTGTGGATGGCTGCCAGAGTCAGGGCTCTTATCCTTCCCTCCTAGAAAGGGTGCAGAGAGATCTCACGTGGCCAAACCACGAGGAGGCAGAAGACAA]GCCGGATCTGTTGTGGCCGTGCCACACCTCATGGGCACCAGCCTGGCTGGGAAGGGCC
AGAGGCAGAGAGGGAAAGATGCTGTCCAGGCTTGGAAAGATTCTGGAAGAAACCTGAGACCG
AATTTAACCCCCCAAGGGATGTGAAAGCGATCATGTCATCGGGATGCAGGCCGTGA
CTCAGCCAGCAGATGGGAGGAACTGGAGAGATCACCTCTACAGGAGGAAGCCAAGAGGT
TCTGGCATCGGTTCATGTTCAGAAAGGGCCGGCGTCCAGGGAGTCAT [CCTGCCCATC
 AAAAGCCACGAAGTACACTGGGAGACCTGCAGGACTGTGCCCTCAACCAG] ACCATTGC
 CCATGAAGACTGTCAAAAAGTCGTGTCCAGAACAACTTTGCTTGGCAAATGCAGTTC
 CATTGTTTCCCGAGAACGGGCAGATGCCACAGCTCTGCTCCACTGCTCGCCAC
 CAAATTACCAACCGTGCACTTGTATGCTGAAGTGCACCCAGGAAACCCCCGTGGTCAAGAT
 GGTGATGCAAGTAGAAGAGTGTCACTGGTGAAGACGGAACGTGGAGAGGAGGCGCT
 CCTACTGGCTGGTCCCAGGGTCTCATCCCTGGACTTCCAGCTTCAAAACAAACCC
 ATGAATTACCTCAACAGAAAGCAAACCTCAACAGAAATAAGTGAGGGTTATTCAATCTGG
 AAATGTTATGTGAGTTATATAAGATCACTGGAAAATATCTTCTCTCCCTCTCTCCC
 CCTCTCTCTCTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 TCACACACACACACACACACACACACACATGTTGTGTTAGACAGGGTCTTAT
 GTATTCTCAGCTGGCTCAAACATGTCAGGGATGTTAAACTCCTGATCC
 AATTCTGAGTGTGGGATTACAGACATGCTCCATAANACATAGCTCCCAGAAGGATTT
 TAAAAGAGATTTGCATGTTCAAAGTTGCTTGTAGACTCAGAAATATTTGATNTATT
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 GTTCGTTCAAGATTCTCCACATGAAGTTTACTGTTGGTATCTGGCGTGAAGAAGGA
 ATAGTGAAGGTACTTTAACAGTTACACCTGGAAGGGCTCAGGCACTAGGAACCAACC
 TTTCCCGGAATATGAGGAAATACATGAACAGTATTAGAGTCACCTGAGGAAGTTACTA
 GGAAACGCCATAAGTCTCCAAGTACATTGTGAGTCATTGAAAGGACAATCGTGTATATA
 GACGAAATCTCTACTCGTATGCTTGAATCTTCTAGCAAGTTAGGTTCTATGTTGG
 GCTTCTCCTATTGCTAAGAGTATGTGTGACAATTCAACCTGACAAATACCTCAATGG
 CAAATTCTGACCCCTG

**Gene Sequence
Structure ***

241 bp

Sequence Deleted

528 bp

Size of full-length
cDNA: 1752 bp

FIGURE 2A

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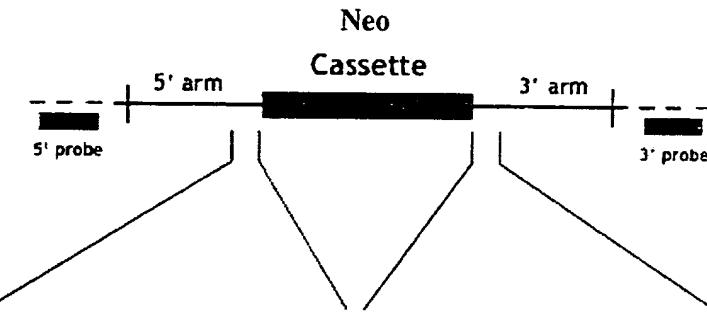
Targeting Vector* (genomic sequence)

Construct Number: 269

Arm Length:

5': 2 kb

3': 1.7 kb



— Targeting Vector

- - - - Endogenous Locus

* Not drawn to scale

5' > TCCATCTGTGAATCTAACCTC
AGTCTCTGGAAATCAGGAAGCATG
CATCTCCTCTTAGTTAGCTCAGCTGCTT
GTTCTCTTGCCTCTGGGAAGGCA
GACCTATGTGTGGATGGCTGCCAG
AGTCAGGGCTCTTATCCTTCC
CTCCCAGAAAGGGTGCAGAGAT
CTCCACGTGCCAACACGAGGGAG
GCAGAAGACAA<3'
(SEQ ID NO: 13)

5' > CCTGCCCATCAAAAGCCACGA
AGTACACTGGGAGACCTGCAGGAC
TGTGCCCTCAACCAGGTATGCAT
TCTAGAGGGTAAACCCACAGCTGGACA
CCAGACAGGGAGGACAGCTGGACA
GCTAGGACAAACGGCAAAATAGAA
AGAGTCTGGCGAGAGCTCGGGCCT
TGTCTAGTTCCAGATTCAAGTCCTT
TGGGTATTCAAT<3'
(SEQ ID NO: 14)

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIGURE 2B

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Phenotypic Data Summary - Open Field

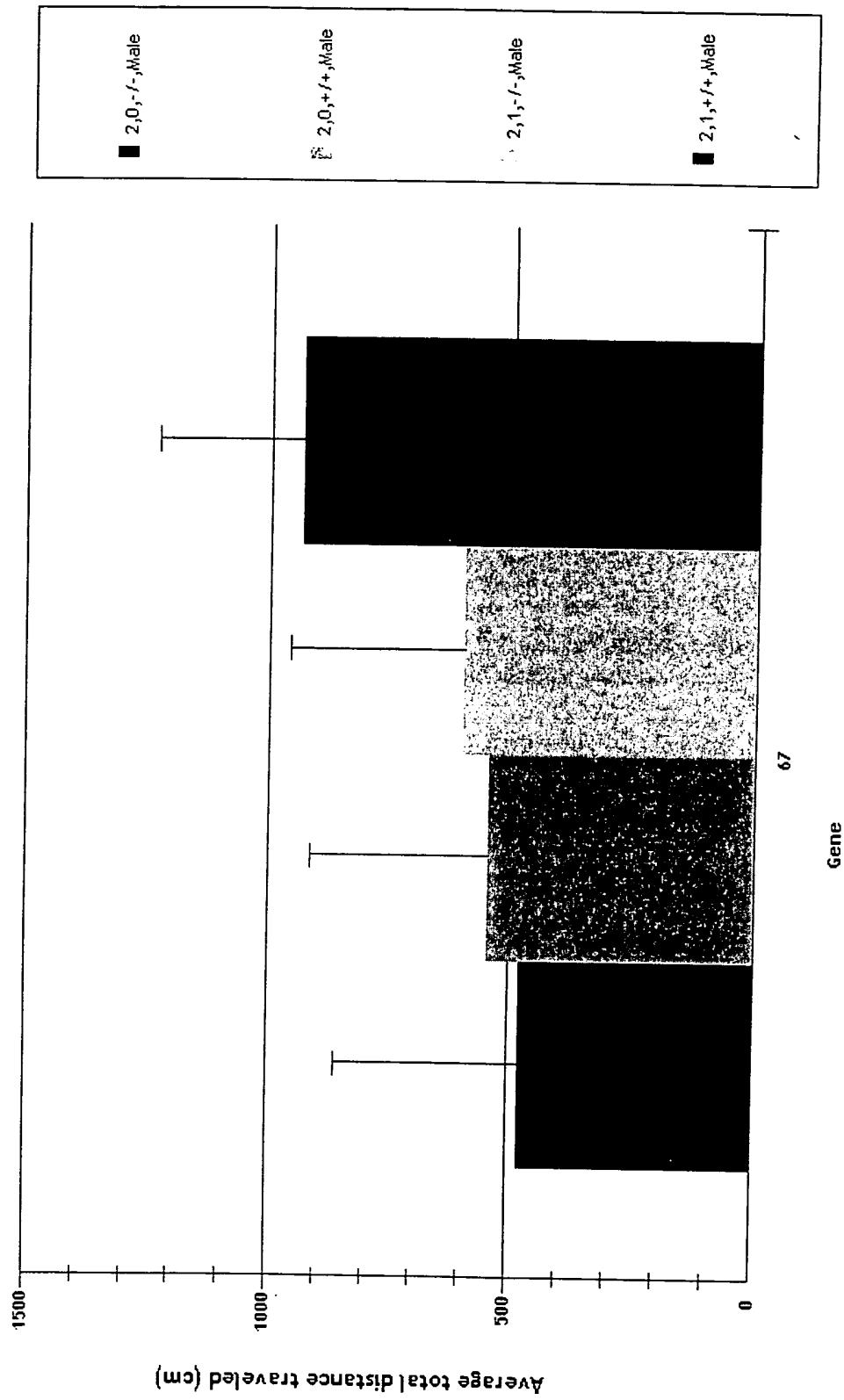


FIGURE 3

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Phenotypic Data Summary - Tail Suspension

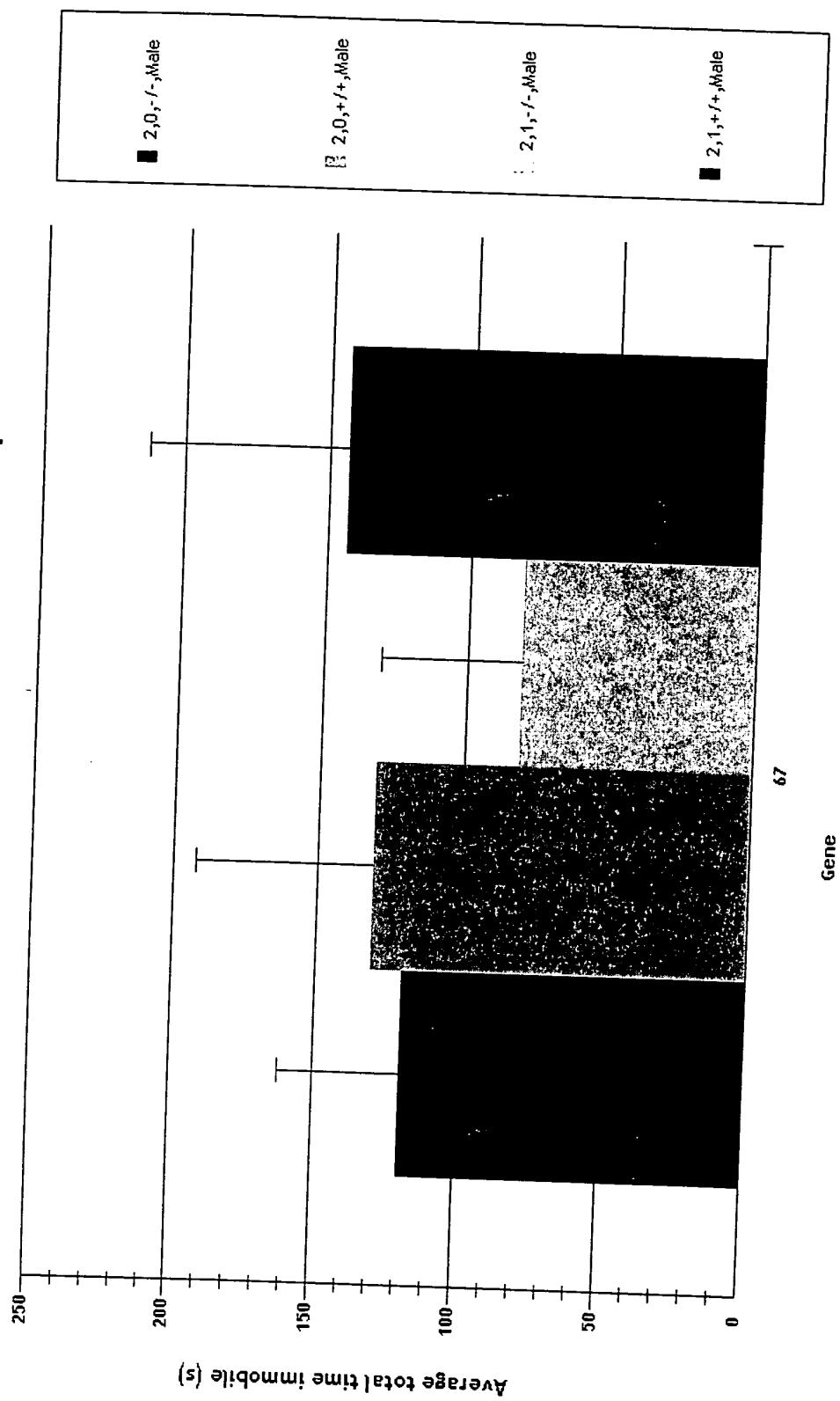


FIGURE 4

Gene

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